

17
9-27-03

1600

RAW SEQUENCE LISTING

DATE: 08/18/2003

PATENT APPLICATION: US/09/834,792C

TIME: 19:00:38

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08182003\I834792C.raw

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3 <110> APPLICANT: Mount Sinai School of Medicine of NYU
5 <120> TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
6   CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
9 <130> FILE REFERENCE: 1270-007
11 <140> CURRENT APPLICATION NUMBER: 09/834,792C
12 <141> CURRENT FILING DATE: 2001-04-13
14 <150> PRIOR APPLICATION NUMBER: 60/197,491
15 <151> PRIOR FILING DATE: 2000-04-17
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: Windows 2000 MS DOS w/ line breaks
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 4157
23 <212> TYPE: DNA
24 <213> ORGANISM: Murine TRP8 cDNA
26 <400> SEQUENCE: 1
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29 ggagagatca acttcggagg gtctgggaag aagcgaggca agtttgtgaa ggtgccaaagc 180
30 agtgtggccc cctctgtgct ttttgaactc ctgctcaccg agtggcacct gccagccccc 240
31 aacctggtgg tgtccctggt gggtagaggaa cgaccttttg ctatgaagtc gtggcttcgg 300
32 gatgtcctgc gcaaggggct ggtgaaagca gctcagagca cagggtgcctg gatcctgacc 360
33 agtgcctccc acgtgggcct ggcccgccat gttggacaag ctgtacgtga tcaactctctg 420
34 gctagcacat ccaccaagat ccgtgtagtg gccatcggaa tggcctctct ggatcgaatc 480
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37 atccttgtgg agtcaggcgc ccttgggagt gggaaacgac ggctgacaga gctgcagctg 660
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39 atacctgtcc tttgcctgtt ggtcaatggt gaccccaaca ccctagagag gatttccagg 780
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57 tgctacggca acagtgaagga ccgtgccttt gccctgctgg tgcgaaggaa ccacagctgg 1860
58 agcaggacca cgtgcctgca cctggccact gaagctgatg ccaaggcctt ctttgcccat 1920
59 gacggtgtgc aagcattcct gaccaagatc tgggtggggag acatggccac aggcacaccc 1980
60 atcctacggc ttctgggtgc cttcaacctg ccagccctca tctacacaaa cctcatctcc 2040
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101 <211> LENGTH: 1158
102 <212> TYPE: PRT
103 <213> ORGANISM: Murine TRP8
105 <400> SEQUENCE: 2
107 Met Gln Thr Thr Gln Ser Ser Cys Pro Gly Ser Pro Pro Asp Thr Glu
108 1 5 10 15

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109 Asp Gly Trp Glu Pro Ile Leu Cys Arg Gly Glu Ile Asn Phe Gly Gly
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111 Ser Gly Lys Lys Arg Gly Lys Phe Val Lys Val Pro Ser Ser Val Ala
112      35      40      45
113 Pro Ser Val Leu Phe Glu Leu Leu Leu Thr Glu Trp His Leu Pro Ala
114      50      55      60
115 Pro Asn Leu Val Val Ser Leu Val Gly Glu Glu Arg Pro Leu Ala Met
116 65      70      75      80
117 Lys Ser Trp Leu Arg Asp Val Leu Arg Lys Gly Leu Val Lys Ala Ala
118      85      90      95
119 Gln Ser Thr Gly Ala Trp Ile Leu Thr Ser Ala Leu His Val Gly Leu
120      100     105     110
121 Ala Arg His Val Gly Gln Ala Val Arg Asp His Ser Leu Ala Ser Thr
122      115     120     125
123 Ser Thr Lys Ile Arg Val Val Ala Ile Gly Met Ala Ser Leu Asp Arg
124      130     135     140
125 Ile Leu His Arg Gln Leu Leu Asp Gly Val His Gln Lys Glu Asp Thr
126 145     150     155     160
127 Pro Ile His Tyr Pro Ala Asp Glu Gly Asn Ile Gln Gly Pro Leu Cys
128      165     170     175
129 Pro Leu Asp Ser Asn Leu Ser His Phe Ile Leu Val Glu Ser Gly Ala
130      180     185     190
131 Leu Gly Ser Gly Asn Asp Gly Leu Thr Glu Leu Gln Leu Ser Leu Glu
132      195     200     205
133 Lys His Ile Ser Gln Gln Arg Thr Gly Tyr Gly Gly Thr Ser Cys Ile
134      210     215     220
135 Gln Ile Pro Val Leu Cys Leu Leu Val Asn Gly Asp Pro Asn Thr Leu
136 225     230     235     240
137 Glu Arg Ile Ser Arg Ala Val Glu Gln Ala Ala Pro Trp Leu Ile Leu
138      245     250     255
139 Ala Gly Ser Gly Gly Ile Ala Asp Val Leu Ala Ala Leu Val Ser Gln
140      260     265     270
141 Pro His Leu Leu Val Pro Gln Val Ala Glu Lys Gln Phe Arg Glu Lys
142      275     280     285
143 Phe Pro Ser Glu Cys Phe Ser Trp Glu Ala Ile Val His Trp Thr Glu
144      290     295     300
145 Leu Leu Gln Asn Ile Ala Ala His Pro His Leu Leu Thr Val Tyr Asp
146 305     310     315     320
147 Phe Glu Gln Glu Gly Ser Glu Asp Leu Asp Thr Val Ile Leu Lys Ala
148      325     330     335
149 Leu Val Lys Ala Cys Lys Ser His Ser Gln Glu Ala Gln Asp Tyr Leu
150      340     345     350
151 Asp Glu Leu Lys Leu Ala Val Ala Trp Asp Arg Val Asp Ile Ala Lys
152      355     360     365
153 Ser Glu Ile Phe Asn Gly Asp Val Glu Trp Lys Ser Cys Asp Leu Glu
154      370     375     380
155 Glu Val Met Thr Asp Ala Leu Val Ser Asn Lys Pro Asp Phe Val Arg
156 385     390     395     400
157 Leu Phe Val Asp Ser Gly Ala Asp Met Ala Glu Phe Leu Thr Tyr Gly

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158                               405                               410                               415
159 Arg Leu Gln Gln Leu Tyr His Ser Val Ser Pro Lys Ser Leu Leu Phe
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161 Glu Leu Leu Gln Arg Lys His Glu Glu Gly Arg Leu Thr Leu Ala Gly
162                               435                               440                               445
163 Leu Gly Ala Gln Gln Ala Arg Glu Leu Pro Ile Gly Leu Pro Ala Phe
164                               450                               455                               460
165 Ser Leu His Glu Val Ser Arg Val Leu Lys Asp Phe Leu His Asp Ala
166 465                               470                               475                               480
167 Cys Arg Gly Phe Tyr Gln Asp Gly Arg Arg Met Glu Glu Arg Gly Pro
168                               485                               490                               495
169 Pro Lys Arg Pro Ala Gly Gln Lys Trp Leu Pro Asp Leu Ser Arg Lys
170                               500                               505                               510
171 Ser Glu Asp Pro Trp Arg Asp Leu Phe Leu Trp Ala Val Leu Gln Asn
172                               515                               520                               525
173 Arg Tyr Glu Met Ala Thr Tyr Phe Trp Ala Met Gly Arg Glu Gly Val
174                               530                               535                               540
175 Ala Ala Ala Leu Ala Ala Cys Lys Ile Ile Lys Glu Met Ser His Leu
176 545                               550                               555                               560
177 Glu Lys Glu Ala Glu Val Ala Arg Thr Met Arg Glu Ala Lys Tyr Glu
178                               565                               570                               575
179 Gln Leu Ala Leu Asp Leu Phe Ser Glu Cys Tyr Gly Asn Ser Glu Asp
180                               580                               585                               590
181 Arg Ala Phe Ala Leu Leu Val Arg Arg Asn His Ser Trp Ser Arg Thr
182                               595                               600                               605
183 Thr Cys Leu His Leu Ala Thr Glu Ala Asp Ala Lys Ala Phe Phe Ala
184                               610                               615                               620
185 His Asp Gly Val Gln Ala Phe Leu Thr Lys Ile Trp Trp Gly Asp Met
186 625                               630                               635                               640
187 Ala Thr Gly Thr Pro Ile Leu Arg Leu Leu Gly Ala Phe Thr Cys Pro
188                               645                               650                               655
189 Ala Leu Ile Tyr Thr Asn Leu Ile Ser Phe Ser Glu Asp Ala Pro Gln
190                               660                               665                               670
191 Arg Met Asp Leu Glu Asp Leu Gln Glu Pro Asp Ser Leu Asp Met Glu
192                               675                               680                               685
193 Lys Ser Phe Leu Cys Ser Arg Gly Gly Gln Leu Glu Lys Leu Thr Glu
194                               690                               695                               700
195 Ala Pro Arg Ala Pro Gly Asp Leu Gly Pro Gln Ala Ala Phe Leu Leu
196 705                               710                               715                               720
197 Thr Arg Trp Arg Lys Phe Trp Gly Ala Pro Val Thr Val Phe Leu Gly
198                               725                               730                               735
199 Asn Val Val Met Tyr Phe Ala Phe Leu Phe Leu Phe Thr Tyr Val Leu
200                               740                               745                               750
201 Leu Val Asp Phe Arg Pro Pro Pro Gln Gly Pro Ser Gly Ser Glu Val
202                               755                               760                               765
203 Thr Leu Tyr Phe Trp Val Phe Thr Leu Val Leu Glu Glu Ile Arg Gln
204                               770                               775                               780
205 Gly Phe Phe Thr Asp Glu Asp Thr His Leu Val Lys Lys Phe Thr Leu
206 785                               790                               795                               800

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207 Tyr Val Glu Asp Asn Trp Asn Lys Cys Asp Met Val Ala Ile Phe Leu
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209 Phe Ile Val Gly Val Thr Cys Arg Met Val Pro Ser Val Phe Glu Ala
210      820      825      830
211 Gly Arg Thr Val Leu Ala Ile Asp Phe Met Val Phe Thr Leu Arg Leu
212      835      840      845
213 Ile His Ile Phe Ala Ile His Lys Gln Leu Gly Pro Lys Ile Ile Ile
214      850      855      860
215 Val Glu Arg Met Met Lys Asp Val Phe Phe Phe Leu Phe Phe Leu Ser
216 865      870      875      880
217 Val Trp Leu Val Ala Tyr Gly Val Thr Thr Gln Ala Leu Leu His Pro
218      885      890      895
219 His Asp Gly Arg Leu Glu Trp Ile Phe Arg Arg Val Leu Tyr Arg Pro
220      900      905      910
221 Tyr Leu Gln Ile Phe Gly Gln Ile Pro Leu Asp Glu Ile Asp Glu Ala
222      915      920      925
223 Arg Val Asn Cys Ser Leu His Pro Leu Leu Leu Glu Ser Ser Ala Ser
224      930      935      940
225 Cys Pro Asn Leu Tyr Ala Asn Trp Leu Val Ile Leu Leu Leu Val Thr
226 945      950      955      960
227 Phe Leu Leu Val Thr Asn Val Leu Leu Met Asn Leu Leu Ile Ala Met
228      965      970      975
229 Phe Ser Tyr Thr Phe Gln Val Val Gln Gly Asn Ala Asp Met Phe Trp
230      980      985      990
231 Lys Phe Gln Arg Tyr His Leu Ile Val Glu Tyr His Gly Arg Pro Ala
232      995      1000      1005
233 Leu Ala Pro Pro Phe Ile Leu Leu Ser His Leu Ser Leu Val Leu Lys
234      1010      1015      1020
235 Gln Val Phe Arg Lys Glu Ala Gln His Lys Arg Gln His Leu Glu Arg
236 1025      1030      1035      1040
237 Asp Leu Pro Asp Pro Leu Asp Gln Lys Ile Ile Thr Trp Glu Thr Val
238      1045      1050      1055
239 Gln Lys Glu Asn Phe Leu Ser Thr Met Glu Lys Arg Arg Arg Asp Ser
240      1060      1065      1070
241 Glu Gly Glu Val Leu Arg Lys Thr Ala His Arg Val Asp Leu Ile Ala
242      1075      1080      1085
243 Lys Tyr Ile Gly Gly Leu Arg Glu Gln Glu Lys Arg Ile Lys Cys Leu
244      1090      1095      1100
245 Glu Ser Gln Ala Asn Tyr Cys Met Leu Leu Leu Ser Ser Met Thr Asp
246 1105      1110      1115      1120
247 Thr Leu Ala Pro Gly Gly Thr Tyr Ser Ser Ser Gln Asn Cys Gly Cys
248      1125      1130      1135
249 Arg Ser Gln Pro Ala Ser Ala Arg Asp Arg Glu Tyr Leu Glu Ser Gly
250      1140      1145      1150
251 Leu Pro Pro Ser Asp Thr
252      1155
257 <210> SEQ ID NO: 3
258 <211> LENGTH: 3498
259 <212> TYPE: DNA

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VERIFICATION SUMMARY

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